

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: May 7, 2002, 12:08:53 ; Search time 19.81 Seconds
(without alignments)
262.817 Million cell updates/sec

Title: US-09-772-103-10
Perfect score: 742
Sequence: 1 MAVLVFLCLVAPPSCVLSQ.....MKRGVAMDYWGQGLTVTVSS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
al number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	506	68.2	144	1 HV43_MOUSE	P01819 mus musculus
2	475	64.0	116	1 HV45_MOUSE	P01821 mus musculus
3	464	62.5	115	1 HV44_MOUSE	P01820 mus musculus
4	415	55.9	135	1 HV02_XENLA	P02957 xenopus lae
5	414.5	55.9	146	1 HV21_HUMAN	P06331 homo sapien
6	390.5	52.6	137	1 HV46_MOUSE	P01822 mus musculus
7	379	51.1	117	1 HV26_HUMAN	P01825 homo sapien
8	376	50.7	129	1 HV2F_HUMAN	P01824 homo sapien
9	366	49.3	136	1 HV01_XENLA	P20956 xenopus lae
10	361	48.7	116	1 HV61_MOUSE	P18532 mus musculus
11	352	47.4	116	1 HV60_MOUSE	P18531 mus musculus
12	342.5	46.2	147	1 HV2H_HUMAN	P04438 homo sapien
13	341.5	46.0	120	1 HV2B_HUMAN	P01815 homo sapien
14	339	45.7	121	1 HV3J_HUMAN	P01771 homo sapien
15	332.5	44.8	126	1 HV3K_HUMAN	P01772 homo sapien
16	332	44.7	113	1 HV47_MOUSE	P01823 mus musculus
17	329.5	44.4	122	1 HV3G_HUMAN	P01768 homo sapien
18	325	43.8	119	1 HV2C_HUMAN	P01816 homo sapien
19	324	43.7	125	1 HV2D_HUMAN	P01817 homo sapien
20	324	43.7	136	1 HV2C_RABIT	P01829 oryctolagus
21	323.5	43.6	117	1 HV16_MOUSE	P18533 mus musculus
22	321.5	43.3	136	1 HV16_MOUSE	P01783 mus musculus
23	316.5	42.7	122	1 HV3H_HUMAN	P01769 homo sapien
24	310	41.8	121	1 HV3H_HUMAN	P01818 homo sapien
25	309	41.6	140	1 HV02_MOUSE	P01746 mus musculus
26	308.5	41.4	114	1 HV2A_RABIT	P01827 oryctolagus
27	307.5	41.4	119	1 HV40_MOUSE	P01810 mus musculus
28	306	41.2	117	1 HV2B_HUMAN	P01828 oryctolagus
29	305	41.1	115	1 HV3D_HUMAN	P01765 homo sapien
30	305	41.1	142	1 HV01_RAT	P01805 rattus norv
31	304.5	41.0	114	1 HV3B_HUMAN	P01763 homo sapien
32	304.5	41.0	119	1 HV37_MOUSE	P01807 mus musculus
33	304.5	41.0	126	1 HV2A_HUMAN	P01814 homo sapien

34	304.5	41.0	137	1 HV11_MOUSE	P01755 mus musculus
35	302.5	40.8	139	1 HV07_MOUSE	P01751 mus musculus
36	302	40.7	116	1 HV05_CARAG	P19181 carassius a
37	302	40.7	119	1 HV31_HUMAN	P01770 homo sapien
38	299	40.3	119	1 HV3L_HUMAN	P01773 homo sapien
39	297	40.0	117	1 HV42_MOUSE	P01812 mus musculus
40	296	39.9	115	1 HV3F_HUMAN	P01767 homo sapien
41	295.5	39.8	116	1 HV3T_HUMAN	P01781 homo sapien
42	294	39.6	138	1 HV48_MOUSE	P03980 mus musculus
43	293.5	39.6	119	1 HV3P_HUMAN	P01777 homo sapien
44	292.5	39.4	116	1 HV1A_RABIT	P01826 oryctolagus
45	292	39.4	120	1 HV03_MOUSE	P01747 mus musculus

ALIGNMENTS

RESULT 1
HV43_MOUSE
ID HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.

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or send an email to license@isb-sib.ch).
CC EMBL: J00491; AAA38121.1; -;
DR EMBL: V00768; CAA24149.1; -;
PIR: A02094; G2MS14.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_v.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; Iq; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 68.2%; Score 506; DB 1; Length 144;
Best Local Similarity 67.4%; Pred. No. 1.6e-43;
Matches 97; Conservative 15; Mismatches 30; Indels 2; Gaps 1;
QY 1 MAVLVFLCLVAPPSCVLSQVQLQESGGLVKRPSTLSLTCVSGFSLTSGYGVWRQPP 60
Db 1 MAVALLFLCLATFPSCILSQVLKESGGLVAPPSLSITCTVSGFSLTSGYGVWRQPP 60
QY 61 GRGLEWLVGVIAGGTTNYNSALMSRLTISKDTSKNQVSKLSSVTAADTAVYYCARGP-- 118
Db 61 GRGLEWLVGVIAGGTTNYNSALMSRLTISKDTSKNQVSKLSSVTAADTAVYYCARGP-- 118

us-09-772-103-10-10.rsp

Mon Jul 1 16:28:04 2002

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SEQUENCE FROM N.A.
MEDLINE=81012133; PubMed=6774258;
Sakano H., Maki R., Kurosawa Y., Roeder W., Toneyawa S.;
Two types of somatic recombination are necessary for the generation
of complete immunoglobulin heavy-chain genes.;
Nature 286:676-683(1980).
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; V00767; GAA24148.1; --
PIR; A02095; HVM514; --
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; Igv; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;
SQ
Query Match 62.5%; Score 464; DB 1; Length 115;
Best Local Similarity 75.7%; Pred. No. 1.8e-39;
Matches 87; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
Qy 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGIVYVWRQP 60
Db 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGIVYVWRQP 60
Qy 61 GKLEWLGVIWAGGTNTNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
Db 61 GKLEWLGVIWAGGTNTNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
Qy 61 GKLEWLGVIWAGGTNTNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
Db 61 GKLEWLGVIWAGGTNTNSALMSRLTISKDTNKNQVSLKSSVTAADTAVYKCA 115
RESULT 4
HV02_XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
Schwager J., Mikoryak C.A., Steiner L.A.;
Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.;
Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
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or send an email to license@isb-sib.ch).
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EMBL; J03632; AAA49791.1; --
PIR; B31933; B31933.
DR

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN <1 18
FT CHAIN 19 135
FT NON_TER 135
FT NON_TER 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732B CRC64;

Query Match
Best Local Similarity 55.9%; Score 415; DB 1; Length 135;
Matches 78; Conservative 24; Mismatches 31; Indels 6; Gaps 2;
QY 4 LVLFCLVAFSCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWQPPGKG 63
DB 3 IFFTFMFSSCLTSQT-LOESGPGTVKPSLSRLTCTVSGFSLTSYHHHVIQPPGKG 61
64 LEWLGVIWAGTTNYSALMSRLTISKDTSKNOVSLKSLSVTAADTAVYYCARGPPHAMM 123
DB 62 LEWLGVIATGSAIADSLANRVITIDNGKQVYLQMGMEVKDTAMTYCAR-----EY 116
QY 124 KRGVADYWGQGLVTVSS 142
DB 117 ASGYNTDYWGQGLVTVTS 135

RESULT 5
HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-II REGION ARH-77 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT repeat sequence in 5' flanking region.;
RT Gene 33181-189(1985).
PRT; A02101; G1HUH2.
HSSP; P01825; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CHAIN 20 146
FT DOMAIN 20 117
FT DOMAIN 118 127
FT DOMAIN 128 146
FT DISULFID 42 115
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match
Best Local Similarity 55.9%; Score 414.5; DB 1; Length 146;
Matches 86; Conservative 13; Mismatches 23; Indels 11; Gaps 2;
QY 17 VLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWQPPGKGLEWLVWAGGTT 76
DB 18 VLSQVQLQWAGLVKPSQTLSTCTVSGFSLTSYGYYVWQPPGKGLEWLVWAGGTT 77

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CHAIN 20 146
FT DOMAIN 20 117
FT DOMAIN 118 127
FT DOMAIN 128 146
FT DISULFID 42 115
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match
Best Local Similarity 64.7%; Score 414.5; DB 1; Length 146;
Matches 86; Conservative 13; Mismatches 23; Indels 11; Gaps 2;
QY 17 VLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWQPPGKGLEWLVWAGGTT 76
DB 18 VLSQVQLQWAGLVKPSQTLSTCTVSGFSLTSYGYYVWQPPGKGLEWLVWAGGTT 77

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CHAIN 20 146
FT DOMAIN 20 117
FT DOMAIN 118 127
FT DOMAIN 128 146
FT DISULFID 42 115
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match
Best Local Similarity 55.9%; Score 415; DB 1; Length 135;
Matches 78; Conservative 24; Mismatches 31; Indels 6; Gaps 2;
QY 4 LVLFCLVAFSCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGYYVWQPPGKG 63
DB 3 IFFTFMFSSCLTSQT-LOESGPGTVKPSLSRLTCTVSGFSLTSYHHHVIQPPGKG 61
64 LEWLGVIWAGTTNYSALMSRLTISKDTSKNOVSLKSLSVTAADTAVYYCARGPPHAMM 123
DB 62 LEWLGVIATGSAIADSLANRVITIDNGKQVYLQMGMEVKDTAMTYCAR-----EY 116
QY 124 KRGVADYWGQGLVTVSS 142
DB 117 ASGYNTDYWGQGLVTVTS 135

RESULT 6
HV46_MOUSE STANDARD; PRT; 137 AA.
ID HV46_MOUSE
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment.";
RL Mol. Immunol. 26:431-434(1989).
RN [2]
RP SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
RT immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148756; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
RT chain of a mouse myeloma protein with anti-hapten activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
CC Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
CC -----
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CC -----
DR EMBL; M27638; AAA61337.1;
DR EMBL; X07880; CAA30727.1;
DR PIR; P01012; AVMS35.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.

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us-09-772-103-10.rsp

Mon Jul 1 16:28:04 2002

Immunoglobulin V region; Signal.

1 18 IG HEAVY CHAIN V REGION MOPC 315.
 19 137 FRAMEWORK 1.
 20 48 COMPLEMENTARITY-DETERMINING 1.
 21 54 FRAMEWORK 2.
 22 68 COMPLEMENTARITY-DETERMINING 2.
 23 84 FRAMEWORK 3.
 24 116 COMPLEMENTARITY-DETERMINING 3.
 25 126 FRAMEWORK 4.
 26 137 BY SIMILARITY.
 27 114 G -> GG (IN REF. 1; CAA30727).
 28 15 G -> H (IN REF. 2).
 29 15 GY -> YG (IN REF. 4).
 30 78 N -> D (IN REF. 4).
 31 102 MISSING (IN REF. 4).
 32 123
 33 137
 34 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 52.6%; Score 390.5; DB 1; Length 137;
 Best Local Similarity 57.3%; Pred. No. 4.6e-32;
 Matches 82; Conservative 18; Mismatches 36; Indels 7; Gaps 3;

QY 1 MAVLVFLCLVAFPCVLSQVQLQESGPGLVKPSQTLSTCTVSGFSLTS-YGVVWVRQP 59
 DB 1 MKVLSLLYLLTAIPG-IMSDVQLQESGPGLVKPSQTLSTCTVSGFSLTS-YGVVWVRQP 59
 QY 60 PKGLEWLGCVTWAGTTNYSALMSRLTISKTSKNOVSLKLSVTAADTAVYVCARGPP 119
 DB 60 PGNKLEWLGFTYDGSNGYNSLKNRYSITRDTSENQFLKLSVTDPTATYICAGDND 119
 QY 120 HAMKRGYAMDYWGQGLTVVSS 142
 DB 120 HL-----YVFDYWGQGLTVVSS 137

Query Match 51.1%; Score 379; DB 1; Length 117;
 Best Local Similarity 62.6%; Pred. No. 5.3e-31;
 Matches 77; Conservative 19; Mismatches 21; Indels 6; Gaps 2;

QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVVWVRQPCKGLEWLGVIWAGGTNNYN 79
 DB 1 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVVWVRQPCKGLEWLGVIWAGGTNNYN 79
 QY 80 SALMSRLTISKTSKNOVSLKLSVTAADTAVYVCARGPPHAMKRGYAMDYWGQGLTV 139
 DB 61 TPLRSRVTLVDTSKNOVSLKLSVTAADTAVYVCARN-----LIAG-CIDVWGQGLTV 114
 QY 140 VSS 142
 DB 115 VSS 117

RESULT 8
 HV2F_HUMAN STANDARD; PRT; 129 AA.
 ID HV2F_HUMAN
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION WHA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 [1]
 SEQUENCE.
 RX MEDLINE=77242302; PubMed=407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the Vh region of a human myeloma
 immunoglobulin (IgG New).";
 RL Biochemistry 16:3412-3420(1977).
 CC [2]
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RP MEDLINE=78066916; PubMed=618887;
 RX Saul F.A., Amzel L.M., Poljak R.J.;
 RA "Preliminary refinement and structural analysis of the Fab fragment
 from human immunoglobulin new at 2.0-A resolution.";
 RT J. Biol. Chem. 253:585-597(1978).
 RL [2]
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 PROTEIN.
 CC PIR: A02100; GIHUNM.
 DR PDB: 7FAB; 31-JAN-94.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 DR Immunoglobulin V region; 3D-structure.
 KW Immunoglobulin V region; 3D-structure.
 MOD_RMS 1 PYRROLIDONE CARBOXYLIC ACID.

Query Match 51.1%; Score 379; DB 1; Length 117;
 Best Local Similarity 62.6%; Pred. No. 5.3e-31;
 Matches 77; Conservative 19; Mismatches 21; Indels 6; Gaps 2;

QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVVWVRQPCKGLEWLGVIWAGGTNNYN 79
 DB 1 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVVWVRQPCKGLEWLGVIWAGGTNNYN 79
 QY 80 SALMSRLTISKTSKNOVSLKLSVTAADTAVYVCARGPPHAMKRGYAMDYWGQGLTV 139
 DB 61 TPLRSRVTLVDTSKNOVSLKLSVTAADTAVYVCARN-----LIAG-CIDVWGQGLTV 114
 QY 140 VSS 142
 DB 115 VSS 117

RESULT 8
 HV2F_HUMAN STANDARD; PRT; 129 AA.
 ID HV2F_HUMAN
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION WHA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 [1]
 SEQUENCE.
 RX MEDLINE=82222235; PubMed=6806818;
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 PROTEIN.
 CC PIR: A02099; D2HUMA.
 DR HSSP: P01825; 7FAB.
 DR GlycoSuiteDB: P01824;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 DR Immunoglobulin V region.
 KW NON_TER 129 129
 FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

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Query Match          49.3%;   Score 366;   DB 1;   Length 136;
Best Local Similarity 53.6%;   Pred. No. 1.2e-29;
Matches 74;   Conservative 23;   Mismatches 35;   Indels 6;   Gaps
6  LFCLVAF-PSCVLGQVLOESGFLGPKVPSOTLSLTCTVSGFSLTGYGVYVWRQPPKGL 64
   : : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
4  IFVIEFFPSLISQT-LOESGFGTVKPSLESRLACTVSGFELSYIYVWRQPPKRL 62
   : : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | |
65 EWIGVWAGGTTNYNSALMSRLTTSKDTSKNOVSLKSLSVTAADTAVVYCARGPPHAMK 124
   | : | : | : | : | | | | | | : : : : | | | : | | | | |
63 EWIGVVRDGTATADSLKKNVTITDKNGKVQLQMGMEVKTAMVYCT---STLAGT 119

```

RESULT	11
HV60_MOUSE	
ID	HV60_MOUSE
AC	P18531;
DC	STANDARD;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG HEAVY CHAIN V REGION M315 PRECURSOR.
DS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Mus.
NCBI_TaxID=10090;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/CJ;
RX	MEDLINE=89279149; PubMed-2499654

us-09-772-103-10.rsp

Mon Jul 1 16:28:04 2002

1 MAVLVFLCLVAPPCVLSQVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 1 MDILCSTLLLTVPGLVSGVNLRESGPAVATHTLTCTFSGLSVNRGMSVSWIRQ 60
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR-- 116
 61 PPGKALEWLVARIDDDDDKYYGTSTLETRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 120
 117 -GPPHAMMKRGYAMDYWGQGT 136
 121 VTMVREVMITSNFADWQGT 141

RESULT 13
 HV2B_HUMAN STANDARD; PRT; 120 AA.
 ID HV2B_HUMAN
 AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION COR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RA "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains";
 RT Biochem. J. 117:641-660(1970).
 RL Biochem. J. 117:641-660(1970).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR; A02089; GIHUCO.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Glycoprotein.
 KW MOD_RES 1 94
 FT DISULFID 22 62
 FT CARBOHYD 62 62
 FT NON_TER 120 120
 FT SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;

Query Match 46.0%; Score 341.5; DB 1; Length 120;
 Best Local Similarity 60.0%; Pred. No. 3e-27; Indels 17; Gaps
 Matches 78; Conservative 11; Mismatches 24;

QY 20 QVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQPGKLEWLVGVIWAGGTNN 77
 DB 1 QVTLRESGPAVATHTLTCTFSGLSVNRGMSVSWIRQ 60
 QY 78 YNSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR-----GPPHAMMKRGYAMDYW 132
 DB 61 YNTSELRITISKDTSKNQVSLKSSVTAADTAVYYCAR-----DTATYYCARITVTPAP-----AGY-MDVW 110

QY 133 GQGLTVTVSS 142
 DB 111 GRGTPVTVSS 120

RESULT 14
 HV3J_HUMAN STANDARD; PRT; 121 AA.
 ID HV3J_HUMAN
 AC P01771;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION HIL.

Query Match 46.2%; Score 342.5; DB 1; Length 147;
 Best Local Similarity 53.9%; Pred. No. 2.9e-27;
 Matches 76; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

1 MAVLVFLCLVAPPCVLSQVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 1 MKVLSLLYLTAPG-ILSDVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116

RESULT 12
 HV2H_HUMAN STANDARD; PRT; 147 AA.
 ID HV2H_HUMAN
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION SESS PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84299107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RA "Rearranged immunoglobulin heavy chain variable region (VH)
 pseudogene that deletes the second complementarity-determining
 region";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 RL PIR; A02090; G2HUCS.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 147
 FT DOMAIN 20 118
 FT DOMAIN 119 132
 FT DOMAIN 133 147
 FT NON_TER 147 147
 FT SEQUENCE 147 AA; 16323 MW; FCBDCB3D00FB6666 CRC64;

Query Match 46.2%; Score 342.5; DB 1; Length 147;
 Best Local Similarity 53.9%; Pred. No. 2.9e-27;
 Matches 76; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

1 MAVLVFLCLVAPPCVLSQVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 1 MKVLSLLYLTAPG-ILSDVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116

RESULT 12
 HV2H_HUMAN STANDARD; PRT; 147 AA.
 ID HV2H_HUMAN
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION SESS PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84299107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RA "Rearranged immunoglobulin heavy chain variable region (VH)
 pseudogene that deletes the second complementarity-determining
 region";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 RL PIR; A02090; G2HUCS.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 147
 FT DOMAIN 20 118
 FT DOMAIN 119 132
 FT DOMAIN 133 147
 FT NON_TER 147 147
 FT SEQUENCE 147 AA; 16323 MW; FCBDCB3D00FB6666 CRC64;

Query Match 46.2%; Score 342.5; DB 1; Length 147;
 Best Local Similarity 53.9%; Pred. No. 2.9e-27;
 Matches 76; Conservative 16; Mismatches 44; Indels 5; Gaps 2;

1 MAVLVFLCLVAPPCVLSQVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 1 MKVLSLLYLTAPG-ILSDVQLQESGPGVLRPOTSLTCTVSGFSLTSYG--VYVVRQ 58
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116
 59 PPGKLEWLVGVIWAGGTNNYSALMSRLTISKDTSKNQVSLKSSVTAADTAVYYCAR 116

RESULT 12
 HV2H_HUMAN STANDARD; PRT; 147 AA.
 ID HV2H_HUMAN
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION SESS PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84299107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RA "Rearranged immunoglobulin heavy chain variable region (VH)
 pseudogene that deletes the second complementarity-determining
 region";
 RT Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 RL PIR; A02090; G2HUCS.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 19
 FT CHAIN 20 147
 FT DOMAIN 20 118
 FT DOMAIN 119 132
 FT DOMAIN 133 147
 FT NON_TER 147 147
 FT SEQUENCE 147 AA; 16323 MW; FCBDCB3D00FB6666 CRC64;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE
RX MEDLINE-79124695; PubMed-420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RL cryoimmunoglobulin IgG Hil.";
RL Biochemistry 18:553-560(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR; A02054; G1HUHL.
DR HSP; P01772; 21G2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT Immunoglobulin V region.
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 45.7%; Score 339; DB 1; Length 121;
Best Local Similarity 50.0%; Pred. No. 5.3e-27;
Matches 62; Conservative 27; Mismatches 31; Indels 4; Gaps 2;

QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYVVRQPPGKGLVGVWAGGT-TNY 78
Db 1 QVQLVAGGQVQPGKSLKSLTASGFTFSNYGMHWRAQAPGKGLVWAVIYNGSTYY 60
QY 79 NSALMSRLTISKDTSKNOVSLKLSVTAADTAVYVCARGPPHAMMKRG--YANDYWGQGT 138
Db 61 GDSVKGRTTISRDNKRLTLMZMNSLRTEADTAVYICARDPD---ILTAFSFDYWGQGLV 117
QY 139 TVSS 142
Db 118 TVSS 121

RESULT 15
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
DT 21-JUL-1986 (Rel. 01, Created)
AC 21-JUL-1986 (Rel. 01, Last sequence update)
IG HEAVY CHAIN V-III REGION KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS
RX MEDLINE-83289131; PubMed-6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN [2]
RP Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-81072295; PubMed-7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RL immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
J. Mol. Biol. 141:369-391(1980).
RL PIR; A02055; G1HUHL.
DR PDB; 2F84; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT TURN 11 12
FT STRAND 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 44.8%; Score 332.5; DB 1; Length 126;
Best Local Similarity 50.8%; Pred. No. 2.4e-26;
Matches 64; Conservative 21; Mismatches 38; Indels 3; Gaps 2;

QY 20 QVQLQESGPGLVKPSQTLSTCTVSGFSLTSYGVYVVRQPPGKGLVGVWAGGT-TNY 78
Db 1 QVQLVESGGGVQPGKSLKSLTASGFTFSNYGMHWRAQAPGKGLVWAVIYNGSTYY 60
QY 79 NSALMSRLTISKDTSKNOVSLKLSVTAADTAVYVCARGPPHAMMKRG--YANDYWGQGT 136
Db 61 ADSVKGRTTISRDNKRLTLMZMNSLRTEADTAVYICARDPD---ILTAFSFDYWGQGLV 120
QY 137 TVSS 142
Db 121 TVSS 126

Search completed: May 7, 2002, 12:08:53
Job time: 451 sec

